

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 19, 2002, 14:59:27 ; Search time 22 Seconds  
(without alignments)

Title: US-08-813-323B-1

Sequence: 1 MESSKKMDAGTLQNPPLK.....IKDDTIFIKVIIVDTSDLPPD 567

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database : PIR\_73: \*

```
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description
No.						
1	2894	100.0	567	2	I49272	CD40 receptor-asso
2	2886.5	96.4	568	2	A55660	CD40 receptor-asso
3	32718	90.8	543	2	S68467	CD40 receptor-asso
4	1189.5	39.7	557	2	JC6359	tumor necrosis fac
5	837.5	28.0	501	2	I61512	TNF receptor assoc
6	812.5	27.1	501	2	S56163	tumor necrosis fac
7	641.5	21.4	416	2	B55659	TNFR-associated pr
8	640	21.4	409	2	AS4750	TNF receptor assoc
9	556.5	18.6	470	2	I38026	MLN 62 protein - h
10	547	18.3	522	2	S71821	probable interleuk
11	523.5	17.5	505	2	T22328	hypothetical prote
12	209	7.0	468	2	A29361	hypothetical prote
13	164	5.5	919	2	B72765	DG17 protein - sll
14	161	5.4	634	2	I49642	hypothetical prote
15	157.5	5.3	1039	2	S18199	estrogen-responsiv
16	156.5	5.2	1218	2	T14265	myosin heavy chain
17	155.5	5.2	609	2	A43966	goldin-245 - mouse
18	155	5.2	1676	2	E7140	nuclear phosphopro
19	152	5.1	1300	2	I53799	probable centromer
20	151.5	5.1	313	2	B96682	CG1 protein - huma
21	151.5	5.1	704	2	A48040	hypothetical prote
22	151	5.0	1085	2	F96712	myosin A (EC 3.4.2
23	150	5.0	658	2	S52696	hypothetical prote
24	149	5.0	1356	2	S32763	myosin heavy chain
25	149	5.0	1957	2	T38077	kinectin 1 - huma
26	147.5	4.9	1690	2	T13030	hypothetical colle
27	146.5	4.9	1816	1	S68960	microtubule bindin
28	146	4.9	1679	2	S48385	laminin alpha-4 ch
29	146	4.9	1727	2	T50073	hypothetical prote
						myosin-like coiled

30	145.5	4.9	94.4	2	S26710	spindle pole body
31	145	4.8	1005	2	A64465	hypothetical protein
32	145	4.8	1201	2	T08603	kinesin-related protein
33	144	4.8	1935	1	S06006	myosin beta heavy chain
34	143.5	4.8	753	2	I51302	myosin heavy chain
35	142.5	4.8	1940	1	A24922	myosin heavy chain
36	141.5	4.7	631	2	JC4298	hyaluronan receptor
37	141.5	4.7	1475	2	T33318	hypothetical protein
38	141.5	4.7	1935	1	A37102	myosin beta heavy chain
39	141	4.7	1940	2	A23320	myosin heavy chain
40	141	4.7	1957	2	A45627	myosin heavy chain
41	140.5	4.7	866	2	H6378	conserved hypothetical protein
42	140.5	4.7	1934	2	I48153	myosin heavy chain
43	140	4.7	624	2	S28418	probable zinc-binding protein
44	140	4.7	879	2	C71083	conserved hypothetical protein
45	140	4.7	1313	2	A48467	myosin heavy chain

## ALIGNMENTS

## RESULT 1

149212

CD40 receptor-associated factor 1 - mouse

C; species: Mus musculus (house mouse)

C:\Accession: T49272  
C:\Date: 13-Mar-1996 #sequence\_revision 13-Mar-1996 #lexl\_change 10 Aug 2000

R:Cheng, G.: Cleary

Science 267, 1494-1498, 1995

A;Title: Involvement of CRAF, a relative of TRAF, in C

A; Reference number: A55960; MUID:95184010; PMID:7533327

A;Accession: 149272

A;status: preliminary  
A;Molecular type: MF

A: Residues: 1-567 <BR>A, molecule type: unknown

A: Cross-references: EMB

C;Genetics:

A; Gene: CRAF1

C; Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology

**C;keywords:** zinc finger

E;48-96/Domain: RING finger homology &lt;RING&gt;

Query Match	100.0%	Score 2994	DB 2	Length 567
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Best Local Similarity 100.0%; Pred. No. 1e-165;

Matches	56/;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Qy	1	MESSKKMDAACTLOPNPPLKQDPORGAGSVLYPQGGYKKEKFKYVEDKJKCKCGRVYL	60
Db	1	MESSKKMDAACTLOPNPPLKQDPORGAGSVLYPQGGYKKEKFKYVEDKJKCKCGRVYL	60
Qy	61	NPQTECGHRCFESCMALLSSSSPKTACOEIITKDKVFKDNCKCKREIATLOYCENEG	120
Db	61	NPQTECGHRCFESCMALLSSSSPKTACOEIITKDKVFKDNCKCKREIATLOYCENEG	120
Qy	121	RGCAQOLTLGHLVLHLKNEQFEELPCLRADCKKRYLRKLDHVEKACKYREATSCHCK	180
Db	121	RGCAQOLTLGHLVLHLKNEQFEELPCLRADCKKRYLRKLDHVEKACKYREATSCHCK	180
Qy	181	SOVPKIRKQKHEDIDPCVYVSCCHKCSVOTLRSELSAHLSBECVNAKSPSCFERYGCV	240
Db	181	SOVPKIRKQKHEDIDPCVYVSCCHKCSVOTLRSELSAHLSBECVNAKSPSCFERYGCV	240
Qy	241	OGTNOQIKAHESAASVAVHVNLLKEMSNSLEKRVSLQNESVEYKKSJQSJLHNDICSEIE	300
Db	241	OGTNOQIKAHESAASVAVHVNLLKEMSNSLEKRVSLQNESVEYKKSJQSJLHNDICSEIE	300
Qy	301	IEROKEMIRNNESKLIHLQRIYIDQAEKJLKLDEIRPFROMNEADSMKSVESJLONRV	360
Db	301	IEROKEMIRNNESKLIHLQRIYIDQAEKJLKLDEIRPFROMNEADSMKSVESJLONRV	360
Qy	361	TELESVDKSAGCAARNTGLTESQJLSRHDOQTJSVYDRIPLADMDLRFQVLETAASYGVLTWK	420
Db	361	TELESVDKSAGCAARNTGLTESQJLSRHDOQTJSVYDRIPLADMDLRFQVLETAASYGVLTWK	420

QY	421	IRDKRRKQAAVNGKTLSTLSYQEPFYGYGYMKCARVYLNDGNGKXGTHLSFPVIMRGE	480
Db	421	IRDKRRKQAAVNGKTLSTLSYQEPFYGYGYMKCARVYLNDGNGKXGTHLSLFPVIMRGE	480
QY	481	YDALLPMPFKOKYTLMLMDGSSRRHLGPAFKPDNSSSFKKPTEGEMNTIASGCEVFVAQT	540
Db	481	YDALLPMPFKOKYTLMLMDGSSRRHLGPAFKPDNSSSFKKPTEGEMNTIASGCEVFVAQT	540
QY	541	VLENGTYIKDDTIFIKVIYDTSLDLP	567
Db	541	VLENGTYIKDDTIFIKVIYDTSLDLP	567

## RESULT 2

CD40 receptor-associated factor 1 - human  
N:Alternate names: CD40-binding protein  
C:Species: Homo sapiens (man)  
C:Date: 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 01-Dec-2000  
C:Accession: A55960; #sequence\_revision 15-Mar-1996 #text\_change 01-Dec-2000  
R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.  
Science 267, 1494-1498, 1995  
A:Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.  
A:Reference number: A55960; MUID:95184010; PMID:7533327  
A:Accession: A55960  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-568 <RSS>  
A:Cross-references: EMBL:U01092; NID:9726087; PIDN:AA50112.1; PID:9726088  
R:Mosialos, G.; Birkenbach, M.; Palamarchill, R.; VanArsdale, T.; Ware, C.; Kieff, E.  
Cell 80, 389-399, 1995  
A:Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for  
A:Reference number: A55649; MUID:95163092; PMID:7859281  
A:Accession: A55649  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-128, 'M', 130-568 <MOS>  
A:Cross-references: GB:019260; NID:9675459; PIDN:AAA65732.1; PID:9675460  
R:Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M.  
J. Biol. Chem. 269, 30069-30072, 1994  
A:Title: A novel RING finger protein interacts with the cytoplasmic domain of CD40.  
A:Reference number: A55135; MUID:95073988; PMID:7527023  
A:Accession: A55135  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-128, 'M', 130-133, 135-404, 'G', 406-568 <HUA>  
A:Cross-references: GB:015637; NID:9595910; PIDN:AAA56753.1; PID:9595911  
C:Genetics:  
A:Gene: CRAF1  
C:Superfamily: CD40 receptor-associated protein GAP-1; RING finger homology  
;49-97/Domain: RING finger homology <RNG>

	Query Match	96.4%	Score 2866.5	DB 2	Length 568
	Best Local Similarity	96.1%	Pred. No. 17e-159		
	Matches 546	Conservative 7	Mismatches 14	Indels 1	Gaps 1
QY	1	MESSKMDAAGTLQNPPLKLPDRGAS-VLVPDGGYKEKFKVTEDYKCEKCRVL	59		
Db	1	MESSKMDSPGALQNPPLKLTTRDSAGTPVFEVDEGGYKEKFKVTEDYKCEKCHVL	60		
QY	60	CNRKOTECGHRPCECSEMAILLSSSPKCTACOEESTIKDKYKNDCCRELLALQVYCRNE	119		
Db	61	CSRKQTECHRCRCESMAILLSSSPKCTACOEESTIKDKYKNDCCRELLALQVYCRNE	120		
QY	120	GRGCAEQTLTGLHLVHLNNECOFEELPCLRADCKEYVLKRDLDRDHYEACKYREATCSHC	179		
Db	121	SRGCAEQTLTGLHLVHLNNDCHFEELPCVRPDCKEYVLKRDLDRDHYEACKYREATCSHC	180		
QY	180	KSGVPEIRIKQKEHDNDPCVYVSGCHRSKYOTLLRSLSAHLSCVAPSTGCFKRYGCV	239		
Db	181	KSGVPEIRIALQKHEIDPCVYVSGCHRSKYOTLLRSLSAHLSCVAPSTGCFKRYGCV	240		

QY	240	FQGNMOQIKAHBASSAVOHVLLKEMNSLSEKQVSLLOÑSVKKNKSISOLHNOICSEPI	299
Db	241	FQGNMOQIKAHBASSAVOHVLLKEMNSLEKKVSLLOÑSVKKNKSISOLHNOICSEPI	300
QY	300	ETEROKEMLRNNESEKIHLQFVIDSOAEKIKELDKETIRPRÖRWEADSMKSSVESLONR	359
Db	301	ETEROKEMLRNNESEKIHLQFVIDSOAEKIKELDKETIRPRÖRWEADSMKSSVESLONR	360
QY	360	VTELESYDKSAGQARNTGILLESQLSRHDOTLSVHDIRLADMIRPÖVLETASVNGVLT	419
Db	361	VTELESYDKSAGQARNTGILLESQLSRHDQMLSVHDIRLADMIRPÖVLETASVNGVLT	420
QY	420	KIRDTKRRKQZAVNGKTLISLQPFYTGIGYKMCARVYLINGDMGKGTHTLSLFYIMRG	479
Db	421	KIRDTKRRKQZAVNGKTLISLQPFYTGIGYKMCARVYLINGDMGKGTHTLSLFYIMRG	480
QY	480	EYDALLPPEFOXKTYLIMMOGSSRRRLGAPFPPDNSSFKKPTGEMNITASGCPEYFAO	539
Db	481	EYDALLPPEFOXKTYLIMMOGSSRRRLGAPFPPDNSSFKKPTGEMNITASGCPEYFAO	540
QY	540	TVLENGTYIKDPTIFIKVIVDTSLDPP	567
Db	541	TVLENGTYIKDPTIFIKVIVDTSLDPP	568

### RESULT 3

CD40 receptor-associated protein CAP-1 - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 08-Dec-2000  
C:Accession: S68467, I53498  
R:Sato, T.; Irie, S.; Reed, J.C.  
FEBS Lett. 358, 113-118, 1995  
A:Title: A novel member of the TRAP family of putative signal transducing proteins bl  
A:Reference number: I53498; MUID:95129692; PMID:7530216  
A:Accession: S68467  
A:status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-543 <SAT>  
A:Cross-references: EMBL:L38509; NID:G695357; PID:AAA68195.1; PID:G695358  
A:Experimental source: tissue-type fetal brain  
C:Genetics:  
A:Gene: CAP-1  
C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology  
C:Keywords: homodimer; signal transduction; zinc finger  
i:49-97/Domain: RING finger homology <RNG>

[illegible]

```

Db 276 EIEROKEMLRNNEKSLIHLQRYIDSOAEKLEIDKEIRSFRRONWBEADSMKSSVESLQNR 335
Oy 360 VEELESDVDASAGAAARNGLLESQSLSRHQOTLSVIDIRLADMDLRFQVLETASYNGVLIW 419
Db 336 VEELESVDASAGAAARNGLLESQSLSRHQOTLSVIDIRLADMDLRFQVLETASYNGVLIW 395
Oy 420 KIRDYKRRKQEAVMGKTLISYQSFPYTGFGYKMCARVYLNGDGMKGTHLSLFFVIMRG 479
Db 396 KIRDYKRRKQEAVMGKTLISYQSFPYTGFGYKMCARVYLNGDGMKGTHLSLFFVIMRG 455
Oy 480 EYDALLPMPFKQKVTLMMDGSSRRHLGDAFKPDPNSSFFKKPTGEMNIIASGCPVFAO 539
Db 456 EYDALLPMPFKQKVTLMMDGSSRRHLGDAFKPDPNSSFFKKPTGEMNIIASGCPVFAO 515
Oy 540 TVLENGTYIKDDTIFIKVIVDTSDDLP 567
Db 516 TVLENGTYIKDDTIFIKVIVDTSDDLP 543

```

## RESULT 4

```

Jc6539
tumor necrosis factor receptor-associated factor 5 homolog - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 18-Aug-2000
C:Accession: Jc6539
R:Milushima, S.; Fujita, M.; Ishida, T.; Azuma, S.; Kato, K.; Hirai, M.; Otsuka, M.; Yam
Gene 207, 135-140, 1998
A:Title: Cloning and characterization of a cDNA encoding the human homolog of tumor necr
A:Reference number: Jc6539; MUID:98172745; PMID:9511754
A:Accession: Jc6539

```

```

A:Molecule type: mRNA
A:Residues: 1-557 <M2>
A:Cross-references: DDBJ:AB000509; NID:g2982670; PIDN:BAA25262.1; PID:g2982671
C:Comment: This protein is involved in transduction of signals from various tumor necros
mptoxin-beta receptor.
C:Genetics:
A:Map position: 1932.3-1941.1
C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C:Keywords: coll: tumor, zinc finger
F:41-90/Domain: RING finger homology <RRN>

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Query Match 39.7%; Score 1189.5; DB 2; Length 557;
Best Local Similarity 43.4%; Pred. No. 1.8e-61;
Matches 232; Conservative 112; Mismatches 170; Indels 21; Gaps 9;

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Oy 41 KFKVTVEDKYKCEKRLVLCNPKQTEGCHRCESCMALIS-SSSPKCTACQESIIKDKV 99
Db 34 QFVERLEERYKCAFCCHSVLHNPHTGCHRCQCHILSLRELNTVPICPVDEKVIKQEV 93
Oy 100 FRDNCCREIILALQYCCNNEGRGCAEQLTGLHLVHLKNECOFEELPLRADCKEKYLK 159
Db 94 FRDNCCREIILALQYCCNNEGRGCAEQLTGLHLVHLKNECOFEELPLRADCKEKYLK 151
Oy 160 DLRDHVEKACKYREATCSHCKSOYPMIKLOKHEPTDCPCVVVSCPHKCSVOTILRSLSA 219
Db 152 DLKHEILASCPKREKCLCYCKKDDVYVILQNHHEMLCEYVFCPPMCA-KIILKTEVDE 210
Oy 220 HLSECVNAPSTCSFKRYGCVFQGTNOQITKAHSAVAOVHNLKEMSNLEKKVSLONE 279
Db 211 HLAVCPREAEQOCPRFKYGCATDKRRNLQDQENHSALREHMLVLEKNVQLEQISDLHKS 270
Oy 280 SVEKNKTSQSLHNOICSEIEIEKQEMLRNNEKSLIHLQRYIDSOAEKLEIDKEIRPF 339
Db 271 LEQVESKTLQALFTIKLEKEFKQADLFKNGSFLPNIQ-VFASHIDKSAMLEAQVHOL 329
Oy 340 -----RONWEADSMKSSVESLQNRVTELESVDKSAQAARNGLLESQSLSRHQOTLSV 393
Db 330 LQWVNOQONKDLRLPMEAVDTQAKITILEND-----QRLAVLEETENKIDHTINI 382
Oy 394 HDIRLADMDLRFQVLETASYNGVLIWIKIRDYKRRKQEAVMGKTLISYQSFPYTGFGYK 453
Db 383 HKAOLSKNEERFKLLEGTGCVNGKLIMKVTDYKMKKREAVDGHYVTSISQSPYTSRCGYRL 442

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Oy 454 CARYVLNGDGMKGKTHLSLFFVIMRGEDALLPMPFKQKVTLMMDGSSRRHLGDAFKP 513
Db 443 CARYVLNGDGMKGKTHLSLFFVIMRGEDALLPMPFKQKVTLMMDGSSRRHLGDAFKP 501
Oy 514 DPNSSFFKKPTGEMNIIASGCPVFAOVTLEN-CTYIKDDTIFIKVIVDTSDDLP 566
Db 502 DPNSSFFKKPTGEMNIIASGCPVFAOVTLEN-CTYIKDDTIFIKVIVDTSDDLP 556

```

## RESULT 5

```

161512
TNF receptor associated factor 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C:Accession: 161512
R:Roche, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
Cell 78, 681-692, 1994
A:Title: A novel family of putative signal transducers associated with the cytoplasmic
A:Reference number: A54750; MUID:94349371; PMID:8069916
A:Accession: 161512
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-501 <RBS>
A:Cross-references: GB:L35303; NID:g532620; PIDN:AAC37662.1; PID:g532621
C:Genetics:
A:Gene: TRAF2
C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C:Keywords: zinc
F:30-78/Domain: RING finger homology <RNG>

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Query Match 28.0%; Score 837.5; DB 2; Length 501;
Best Local Similarity 33.5%; Pred. No. 3.4e-41;
Matches 194; Conservative 88; Mismatches 198; Indels 99; Gaps 16;

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Oy 7 MDAAGTQPNPPLKLOPDRGAGSVLPEQGYKEKFKVT-VEDKYKCEKRLVLCNPKQ 65
Db 1 MAAAVTSPGSLLELP-----GFSKTLTGLTLEAKYLCASCKNILRRPQA 47
Oy 66 ECGHRCESCMALISSSPKCTAC-----QSIIT---KDKFKNCCREIILALQYVC 116
Db 48 QCGHRCESCMALISSSPKCTAC-----QSIIT---KDKFKNCCREIILALQYVC 107
Oy 117 RNBGRGCAEQLTGLHLVHLKNECOFEELPLRADCKEKYLKRDLDHVEKACKYREATC 176
Db 108 RNBGRGCAEQLTGLHLVHLKNECOFEELPLRADCKEKYLKRDLDHVEKACKYREATC 163
Oy 177 SHKSOYPMIKLOKHEPTDCPCVVVSCPHKCSVOTILRSLSAHLSECVNAPSTCSFKRY 236
Db 164 SHKSOYPMIKLOKHEPTDCPCVVVSCPHKCSVOTILRSLSAHLSECVNAPSTCSFKRY 221
Oy 237 GCVFQGTNOQITKAHSAVAOVHNLKEMSNLEKKVSLONE 279
Db 222 GCVFQGTNOQITKAHSAVAOVHNLKEMSNLEKKVSLONE 278
Oy 287 IOSLHNOICSEIEIEKQEMLRNNEKSLIHLQRYIDSOAEKLEIDKEIRPFRRQWBEA 346
Db 279 IATFENIVCYLREVER-----VAATVACSCSRHRLDQ----- 312
Oy 347 DSMKSSVESLQNRVTELESVDKSAQAARNGLLESQSLSRHQOTLSVIDIRLADMDLRFQ 406
Db 313 DSMKSSVESLQNRVTELESVDKSAQAARNGLLESQSLSRHQOTLSVIDIRLADMDLRFQ 403
Oy 407 VLETSYNGVLIWIKIRDYKRRKQEAVMGKTLISYQSFPYTGFGYKMCARVYLNGDGMKG 466
Db 344 ELEVTYIDGVTIKIDFTFKRKQEAVAGRPALFSAFTSRKGYKMCARVYLNGDGMKG 403
Oy 467 GTHLSLFFVIMRGEDALLPMPFKQKVTLMMDGSSRRHLGDAFKPDPNSSFFKKPTGE 526
Db 404 GTHLSLFFVIMRGEDALLPMPFKQKVTLMMDGSSRRHLGDAFKPDPNSSFFKKPTGE 462
Oy 527 MNIASCPVFAOVTLEN-NGTYIKDDTIFIKVIVDTSDDLP 564
Db 527 MNIASCPVFAOVTLEN-NGTYIKDDTIFIKVIVDTSDDLP 564

```

Db 463 MN1ASGCLFPCVSKMEAKNSYVDDALFIKAIYDLTGL 501

# RESULT 6

S56163

tumor necrosis factor type 2 receptor associated protein - human

N:Alternate names: TNF receptor-associated protein  
C:Species: Homo sapiens (man)  
C:Date: 10-Oct-1995 #sequence\_revision 01-Dec-1995 #text\_change 03-Nov-2000  
C:Accession: S56163; S58925; S58926; I38729

R:Song, H.Y.; Donner, D.B.

Biochem. J. 309, 825-829, 1995

A:Title: Association of a RING finger protein with the cytoplasmic domain of the human

A:Reference number: S56163; MUID:95366958; PMID:7639698

A:Accession: S56163

A:Molecule type: mRNA

A:Residues: 1-501 <SON1>

A:Cross-references: EMBL:U12597; NID:975272

R:Song, H.Y.; Donner, D.  
submitted to the EMBL Data Library, July 1994

A:Description: Association of a RING finger protein with the cytoplasmic domain of the

A:Reference number: S58925

A:Accession: S58925

A:Molecule type: mRNA

A:Residues: 1-42,63-342,363-501 <SON2>

A:Cross-references: EMBL:U12597; NID:975272

A:Accession: S58926

A:Molecule type: mRNA

A:Residues: 1-342, 'RPPQACGHRYSFCLASIT', 363-501 <SON3>

A:Cross-references: EMBL:U12597; NID:975272; PIDN:AAA87706.1; PID:975273

R:Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.  
Cell 78, 681-697, 1994

A:Title: A novel family of putative signal transducers associated with the cytoplasmic

A:Reference number: A54750; MUID:94349371; PMID:8069916

A:Accession: I38729

A:Status: preliminary: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-342, 'RPPQACGHRYSFCLASIT', 363-501 <ROT>

A:Cross-references: EMBL:U12597; NID:975272; PIDN:AAA87706.1; PID:975273

C:Gene: GDB:TRAF2; TRAF

A:Cross-references: GDB:6268629; OMIM:601895

A:Map position: 9q34-q34

C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology

C:Keywords: zinc finger

F:30-78/Domain: RING finger homology <RNG>

Query Match 27.1%; Score 812.5; DB 2; Length 501;  
Best Local Similarity 33.7%; Pred. No. 9,6e-40;  
Matches 197; Conservative 92; Mismatches 185; Indels 111; Gaps 21;

Db 7 MDAAGLORPPKLQDPDAGAGVLPBQGYKKEKVKVKT-VEDKXKCEKRLVLCNPKQT 65  
1 MAASVTPPGSTELLQ-----GFSKTLTGKLEKTKYCSACRYVLRPRFOA 47  
QY 66 ECGHRCESCMALLSSSPKCTAC-QESIIKDKV-----FKDNCCKEITLALQVYC 116  
Db 48 QGCHRRCSCLASILSSGPNCAVHEGIEYEGISITLSSSAFPMARREVESIPAVC 107  
QY 117 RNRGCAEDLILGHLIVHKNECFEELPCLRAD---CKEYLRKDLADHYEKACKYRE 173  
Db 108 PSD--GCTWAGTLKEY-----ESCHGRCPLMTTECPACKGLVRLGKEKRLHEECPEPS 160  
QY 174 ATGSHCKSVPMIKLOKHEDTDCPCVVVSGPHKCSYQTLIRSELTAHLSECVNAPSTCSF 233  
Db 161 LSCRHCRAPCCGADVKRHHNFV-CPKPLPIC-DGCGKKTIREFQDHVATCGCGRCPCRF 218  
QY 234 KRYGCV--FOGTMOIKAHBSASAVOYVNLKEMSNLEK-----VSLQN-ES 280  
Db 219 HAIGCLETVEGKQO--EHEVQWLRHILAML--LSSVLEAKPLLDGSHAGSELLGRCS 274  
QY 281 VEKNSIQSLHNOICSEFIEIEROKEMLRNNEKIIHLQVINDISOAEKLEKELDKETPRFR 340

Db 275 LEKKA--TPENIVCVLNREVER-----VAMTAACS-----R 305  
QY 341 ONNEADSMKSVESLONRTTELESVDKSGAQAARNTGLLESOLSRHDQTLVHYDIRLAD 400  
Db 306 QHRLDQ---KTEALSSKVOLE-----RSIGIKDLAMD 337  
QY 401 MDLRFVLETASYNGVLIWKIRIDYKRRKQEAANGKTLISYSDPYTYGYGYKMCARVYN 460  
Db 338 LEQKVLMEASTYDGVIMKISDPKRLQEAAGRIPIAFSPAFYTSRYGKMKCRITLYN 397  
QY 461 GDGCKGKTHLSLFFVIMRGEYDALLPFPFKQKTYLMLMDGSSRRRLGDAFKDPNSSF 520  
Db 398 GDGCKGKTHLSLFFVIMRGEYDALLPFPFKQKTYLMLMDGSSRRRLGDAFKDPNSSF 456  
QY 521 KKPTGEMNIASGCPVFAQVYLE-NGTYIKDPTIFKIVYDSDL 564  
Db 457 QRPVNDNIASGCLFPCVSKMEAKNSYVDDALFIKAIYDLTGL 501

# RESULT 7

TNFR-associated protein EB16 - human

C:Species: Homo sapiens (man)

C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 08-Oct-1999

C:Accession: B55649

R:Mostafaei, G.; Birkenbach, M.; Valamanchi, R.; Vanarsdale, T.; Ware, C.; Kieff, E.

Cell 80, 389-399, 1995

A:Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins

A:Reference number: A55649; MUID:95163092; PMID:7859281

A:Accession: B55649

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-416 <MOS>

A:Cross-references: GB:U19261; NID:9675461; PIDN:AAA62309.1; PID:9675462

Query Match 21.4%; Score 641.5; DB 2; Length 416;

Best Local Similarity 35.3%; Pred. No. 5,8e-30;

Matches 165; Conservative 71; Mismatches 126; Indels 103; Gaps 17;

QY 137 KNECFEELPCLRADCKEYLRKDLRHYEKACKYREATCSHCKSQVPMIKLOKHEDTDC 196  
Db 15 ENERPFGCPPTVCDPKPE-----RALCAGCLESNP-----RNGEDQIC 54  
QY 197 PCVVVSCPHKCSVQTL-----LRSELAHSECVNAPSTCSFKRYGCVPGTNOQIK 248  
Db 55 P-----KCRGEDLIQISPGSRLRTOEKAH-PEVAEAGIGCFAGVGGSPQSVQ 105  
QY 249 AHEASSAYOHVNL-----KEMS-----NSLEKYSLLQ-NESEYKNSIQ-SLH 291  
Db 106 EHEVTSQTSNLTLLGFKQKAKRLGCGLESQPALEONLSDLQDAVEAGDLEVDY 165  
QY 292 NQCSFEIEIEROKEMLRNNEKIIHLQVINDISOAEKLEKELDKETIRPFRONNEBADSMS 351  
Db 166 RAPCS-----ESQEE-----LALQHFV--KEKLLAELEGKLRVAF-----E 198  
QY 352 SVESIQNRVTELESYDKSAGAAARTGLLESQLSRH-----DOTLVHDIRLA 399  
Db 199 NIVAVLNEVE-----ASHLALATSLHQSULDRERILLSEQRVELLOOTLACKDQALG 251  
QY 400 DMDLRFVLETASYNGVLIWKIRIDYKRRKQEAANGKTLISYSDPYTYGYGYKMCARVYL 459  
Db 232 KLEOSLRIMEBRSFPGTLMKTIWTRCHHSAGCRIVSLSPAFYTAKEYKICLRLYL 311  
QY 460 NGDGKKGKTHLSLFFVIMRGEYDALLPFPFKQKTYLMLMDGSSRRRLGDAFKDPNSSF 519  
Db 312 NGDGKKGKTHLSLFFVIMRGEYDALLPFPFKQKTYLMLMDGSSRRRLGDAFKDPNSSF 370  
QY 520 FKPTGEMNIASGCPVFAQVYLE-NGTYIKDPTIFKIVYDSDL 562  
Db 371 FORPSETNVASGCLFPPSLKLOSPKHAIVYKDDTMFLKCIYETS 415

RESULT 8

F:14-63/Domain:RING finger homology <RRN>

Query Match 18.6%, Score 556.5; DB 2; Length 470;  
Best Local Similarity 24.1%; Pred. No. 5.5e-25;  
Matches 142; Conservative 80; Mismatches 174; Indels 193; Gaps 12;

```
QY 37 GYKEKFTVTEVDKYKCEGCRVLVCNPKQ-TTEGHHFFCSCMAALLSSSSPKTCAQESTI 95
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 3 GFDYFELKPKRRLLCPICGCKRMREPVYSTGSHAFCDTCLQEFLESEGFKCPEDQLPLD 62
QY 96 KDKVKNDCCKREIATLQVYCNENEGRCAEQLTGLHLLVHLKNECFLELPC----- 147
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 63 YAKITPDELELYQVIGLIRICLHSEGGCRWSGPLKHLQHL-NTCSFNVIQCPNRCPKML 121
QY 148 -----LRADCKE-----KVLKRDLR 162
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 122 SRRLPRLHLQHCPRKRLCKEFCGCGDGEAVESHGMCPOESVYVCENKCGARMRGLLA 181
QY 163 DIVEKACCYREATYTCCHCKSQVPMITKQKHEDTDCCVYVSCPHKCSYQTLRSELNHL 222
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 182 QHATSECKRPQPCYTCKEFEVFDITQSHQ-YQCPRLPACPNOCGVGTVAREDLPGHLK 240
QY 223 E-CVNAPESTCSPKRYGCVFQGNQOIKAHMSAAVQHNVLKEMSNLEKKVSLQNESY 281
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 241 DSCNTALVLCPFKDSGCHNRCKPLMARHVESVPHLAM----- 281
QY 282 EKNKSIQSLHNOICSPFEIIEIRQKEMLRNNEKILQLQVIDSOAEKLELDKEIRPFRQ 341
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 282 -----CA-----LVSQHQQLQELKREL----- 299
QY 342 NMEEADSKSSVESLQNRVTELESVDKSAQAARNTGLLESQLSKHDDTSLVHDIRLADM 401
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 300 -----BELSV----- 304
QY 402 DLRFQVLEFASVNGVLIWKIRIDYKRRKQEAVMGKTLISLOPYTGYGFKCARVYLNG 461
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 305 -----GSDGVLLMKIGSYGRRLQEAKKPKMLECFSPAFYHKYGLQVSAFLNG 354
QY 462 DGMGKGTLSLFEVYLMREBYDALLPMPFKOKVTLMIMDQ-----SSRHLGDAFKPPDPS 517
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 355 NGSGGGHTLSLIRVLPGAPFMLEMPFARRYTSLDQSDPGCLAKPQHVETTFPHDPNW 414
QY 518 SSEKFP-----TGEMNTASGCPVVAQTVLENGTYIKDDTIFIVYD 560
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 415 KNFGPCGTWRGSLDESSLGFGYPKFISHODIKRMYVYRDAVFIKAAVE 463
```

RESULT 10

S71821  
probable interleukin 1 signal-transducing protein TRAF6 - human  
C:Species: Homo sapiens (man)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 02-Sep-2000  
C:Accession: S71821; S71850  
R:Caao, Z.; Xiong, J.; Takeuchi, M.; Kurama, T.; Goeddel, D.V.  
Nature 383, 443-446, 1996  
A:Title: TRAF6 is a signal transducer for interleukin-1.  
A:Reference number: S71821; MUID:96434892; PMID:8837778  
A:Accession: S71821  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-522 <CAO>  
A:Cross-references: EMBL:U78798; NID:g1732425; PIDN:AAB38751.1; PID:g1732426  
R:Caao, Z.; Xiong, J.; Takeuchi, M.; Kurama, T.; Goeddel, D.V.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: S78550  
A:Accession: S78550  
A:Molecule type: mRNA  
A:Residues: 1-275, 'A', 277-522 <CAW>  
A:Cross-references: EMBL:U78798; NID:g1732425; PIDN:AAB38751.1; PID:g1732426  
C:Genetics:  
A:Gene: TRAF6  
C:Function:  
Description: activates transcription factor NF-kappa-B in response to interleukin-1

A: Note: interleukin-1 induces the association of TRAF6 with the IRAK serine/threonine kinase  
 C: Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology  
 C: Keywords: signal transduction; zinc finger  
 F: 66-114/Domain: RING finger homology <RRN>

Query Match 18.3%; Score 547; DB 2; Length 522;

Best Local Similarity 26.6%; Pred. No. 2.2e-24; Mismatches 201; Indels 96; Gaps 16;

Matches 144; Conservative 101; Mismatches 201; Indels 96; Gaps 16;

29 SVLVEPOGQYKKEFKVTEDEYKCEKRLVLCNPKTEGHRFCSCMAALLSSSPKCT 88  
 47 SSFMEIGDYDEPPEPPLESKEGICLMALREAVQTPGCRFKACITKIRAGHNCPL 106  
 89 ACQESITDKYFKKNCCKREIILAOVYCRNGRGCAEDLTGLHLVHLNKEQFEELPCL 148  
 107 VDNELLRLNQLPDDNFARREILSLWKPNE--GCILHKEMLRHEDH-QAHCEPALMDC- 162  
 149 RADCKEVLKRDNRHVERKACKYREATGSHCKSOVPMIKLOKHEDTDCPVVYSCPHKCS 208  
 163 -PCCORPPQKEKINIHITKDCPRROVSCDNCAASMAFEDKEIH-DONCPLANVICER-CN 219  
 209 VQTLRLSELGAHL-ECVNAESTSCFKRYGCVFGTNOQIKAHASSAVOHVNLKEMSN 267  
 220 T-ILIREQMPNHYDLDCPTAPICPTGFGCHKKQNRHRLARHLOENTQSHRMILAQPVH 278  
 268 SLEKRVSLQNESVKNKSTOSLHNOICSFETIEIEROKEMLRNNEKSLIHLQVIDSQAE 327  
 279 SL-----SVLPDSGYIS--EVNRFQETIHQLEGRVLRQDHQIRELTAKMETQSM 325  
 328 KLKELKEIRPFRRNWEADSMKSSVESLQNRVTELESVSAGQAARNTGLLESQLSRH 387  
 326 YVSELRKTRIR-----TLDEKVAEIER----- 346  
 368 DQTLVSHDIRLADMRLRFQVLETSYNGVILWKIRDY---KRRKQEAVMKGTLSLYSQP 443  
 347 -----QQCANGIYIKIGNFEMHKLQCEEE---KPVYIHSFG 379  
 444 EYTGFGYKMCARVYLN-GDGMKGTHLSLFVIMRGFYDALLPMPFKQKTYLMLMOGS 502  
 380 FTTGKPGYKLCRHLQLPTAORCANYISLFTWQGEYDSHLMPPTGGTIRLTITLDOSE 439  
 503 S--RRHLDAKFPDNNSSFFKPTGEMNIAS-GCPVEVAQTVLENGTYIKDFTFIKIY 559  
 440 AVPRQNHHEIMDAKPELLAFQRTIPRNPCKFGVYTFEHLALQRTIKNDITLVNCEV 499  
 560 DT 561  
 500 ST 501

RESULT 11

hypothetical protein F4562.6 - Caenorhabditis elegans

C: Species: Caenorhabditis elegans

C: Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000

C: Accession: T22238

R: Lindsay, S. The EMBL Data Library, March 1997

submitted to the EMBL Data Library, March 1997

A: Reference number: Z19535

A: Accession: T22238

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA

A: Residues: 1-509 <WIL>

A: Cross-references: EMBL:Z93382; PIDN: CAB07615.1; GSPDB: GN00021; CESP: F4562.6

C: Gene: CESP: F4562.6

A: Map position: 3

A: Introns: 94/2; 119/3; 201/3; 223/3; 249/1; 277/3; 300/3; 327/3; 360/1; 395/3; 448/3

C: Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology

F: 61-107/Domain: RING finger homology <RRN>

Query Match 17.5%; Score 523.5; DB 2; Length 509;

Best Local Similarity 26.2%; Pred. No. 4.8e-23; Mismatches 137; Conservative 68; Mismatches 188; Indels 129; Gaps 12;

52 CERKRLVLCNPKQTEGHRFCSCMAALLSSSPKCTACQESTIKDKVFNCKRELLA 111  
 65 CPICEQALRPPIKLNCDHNHCRCQFEN--ENRTPGCAQCTIQLPQLCQHDRAKQQLIA 122  
 112 LQVYCRNREGGCAEDLTGLHLVHLNKEQFE-ELPCLRADCKEYLRKDLRDHKEACK 170  
 123 LPVYCTFEESGCPWDQGLTGLHDHL-SECTFKSSLCEK--CGRQPAKNDLEKHNRAK-CE 178  
 171 YREATGSHCKSOVPMIKLOKHEDTDCPVVYSCPHKCSVQTLRLSELGAHLSECVAPST 230  
 179 LNRVAVCSFCKKTIKDSREHNPRT-CPQVYISCPFGGLDRPRLTEAHCSQPNVNV 237  
 231 CSFKRYGCVFGTNOQIKAHASSAVOHVNLKEMSNLEKRVSLQNESVKNKSTOSL 290  
 238 CPVYVYCTFEESGCPWDQGLTGLHDHL-SECTFKSSLCEK--CGRQPAKNDLEKHNRAK-CE 283  
 291 HNOICSFETIEIEROKEMLRNNEKSLIHLQVIDSQAEKLKELDKELRPFRRNWEADSMK 350  
 284 -----ERDMGSFNDROTIRL-----SAAETCTEM----- 307  
 351 SSVESLQNRVTELESVDSKAGQAARNTGLLESQLSRHQDQLSVHDIRLADMRLRFQVLET 410  
 308 ----- 307  
 411 ASYNGVILWKIRDYKRRKQEAVMKGTLSLYSQPFGYGYKMCARVYNGDMKGTHL 470  
 308 -FGPQLIMKIDKLOQRTNEAKSGADTTTFVSFPMHSRGYKMACACLFSGSSAGKSI 365  
 471 SLEFVIMRGFYDALLPMPFKQKTYLMLMOGS-----SRHLGDAFKRDPNNSKPKRT 524  
 366 SLVYLLKLGHEFDLPLEPFHRAKISLDDNPREDRVNTIYVDRKILAKNEKELAPR 425  
 525 GEMNIASGCPVEVAQTVLENGTYIKDFTFIKIYVPTSD-LP 565  
 426 GERMAAGSOFCSLALON--YVKDKITVQDIDVRCETLP 465

RESULT 12

DG17 protein - slime mold (Dictyostelium discoideum)

C: Species: Dictyostelium discoideum

C: Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 29-Oct-1999

C: Accession: A29361

R: Driscoll, D.M.; Williams, J.G.

Mol. Cell. Biol. 7, 4482-4489, 1987

A: Title: Two divergently transcribed genes of Dictyostelium discoideum are cyclic AMP

A: Reference number: A29361; MID: 88142840; PMID: 2830496

A: Accession: A29361

A: Molecule type: DNA

A: Residues: 1-458 <DRI>

A: Cross-references: GB:M18106; MID: 9167729; PIDN: AAA33192.1; PID: 9167730

C: Keywords: DNA binding; zinc finger

Query Match 7.0%; Score 209; DB 2; Length 458;

Best Local Similarity 20.3%; Pred. No. 6.3e-05; Mismatches 115; Conservative 80; Mismatches 177; Indels 194; Gaps 27;

47 EDYKCEKRLVLCNPKQTEGHRFCSCMAALLSSSPKCTACQ-----EST 94  
 22 KNTYTPDICEFIYKQIYCKSGHACKCEWKEKSLTKK-ECMTKCSVYNSYNDLSRL 80  
 95 IKDKVF--KDNCC--KREIILAOVYC-----RNEGRCACADLTGLHL 133  
 81 MVERAPDKKCCCIYSPNEDYVSGTNCSPDQASVQGNRLIKDENCKCKEIEVDQD 140  
 134 VHLNKEQFEELPCLRADCKEYLRKDLRDHKEACKYRPAQCSHCK-SQVPMIKLOKHE 192  
 141 SHLIN-QQYKTVYCSFKG-EKILR--MNSIKMNGFRLVYCDCKRDKIDKKKELETHY 195





J. MOL. EVOL. 33, 357-366, 1991

A;Title: Structural and phylogenetic analysis of the chicken ventricular myosin heavy chain  
A;Reference number: 518189; MIMD:021303260; PMID:17747288

A/Accession: S18199

A;Accession: S18199

A;Status: preliminary  
A:Molecule type: mRNA

A;Residues: 1-1039 <STE>

A;Residues: 1-1039 &lt;STE&gt;

A:Note: in the authors' translation 45-Ivs is shown after residue 40, an  
A;Cross-references: EMBL:X59552; NID:g62995; PDBN:CAA42130.1; PID:g62996

C; Superfamily: myosin heavy chain; myosin motor domain homology

F:402-409/Region: nucleotide-binding motif  
C:Keywords: ATP; nucleotide binding; P-100pp  
E:402-409/Region: nucleotide-binding motif

F;402-409/Region: nucleotide-binding motif

F;402-409/Region: nucleotide-binding motif A (P-loop)

Query Match	Score	DB 2	Length
5.38;	157.5;	DB 2;	Length 1039;

Best Local Similarity 20.1%; Pred. No. 0.16;  
Matches 102; Conservative 85; Mismatches 184; Indels 137; Gaps 21.

Matches 102; Conservative 85; Mismatches 184; Indels 137; Gaps 21;

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QY 14 QPNPPLKLOPDRGAGSVLPEEGGKKEKFKVTEDKYEKCKRCLVLCNPKEGCHHFC 73
      | : : | : : | : : | : | :
DB 528 QEDMDIDLEKANSAAASLDKKGRGF-DPIINDMKQYEESQAEI-----EASQKEAR 578

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DB 328 QEDMMIDLEKANSAAASLUKKQKGF-DKLLINDMKQKYEESQJAELEASQKEAK 3/6

QY 74 SCMAALLSSSPKCTACQESI IKDKVFKDNCCKREILALQVYCRNEGRGCAEQTLGHL 133

Db 579 SLSTFLFKLN---AYEETL-DHL---ETLKRENKLNQ---EEISDLTNQISEGKKN 625

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QY      134 VH-----LKNECQFE-----ELPCLRADCKEVLRKD-- 160

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Db 626 THEIEKYKQVEQEKSEVQLALEAEAGALEHESKTLRFQLELSQKADFERKLAEKDEE 685

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161  --LRDHVEKACKYREATC-SHCKSQVPMIKLQKHEDTDCPCVVVSCPH----- 205
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